

3707

1
SEQUENCE LISTING
APR 2006

<110> Yarden, Yosef
Amit, Ido
Yakir, Liat

<120> POLYNUCLEOTIDES, POLYPEPTIDES AND ANTIBODIES AND USE THEREOF IN
TREATING TSG101-ASSOCIATED DISEASES

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<170> PatentIn version 3.2

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840

845

Ile Thr Leu Asp Met Leu Ser Arg Met Gly Pro Gly Asp Leu Ala Lys
 850 855 860

Val Gly Val Ser Glu Ala Gly Leu Gln His Glu Ile Leu Arg Arg Ala
 865 870 875 880

Arg Asp Leu Leu Asp Val Ala Arg Val Gln Pro Glu Leu Lys Pro Pro
 885 890 895

Lys Asn Glu Val Phe Gly Val Ser Glu Pro Pro Thr Ala Pro Gln Glu
 900 905 910

Leu Pro Glu Ser Val Arg Pro Ser Ala Pro Pro Ala Glu Leu Asp Val
 915 920 925

Pro Thr Ser Glu Cys Val Val Cys Leu Glu Arg Glu Ala Gln Met Val
 930 935 940

Phe Leu Thr Cys Gly His Val Cys Cys Cys Gln Gln Cys Cys Gln Pro
 945 950 955 960

Leu Arg Thr Cys Pro Leu Cys Arg Gln Glu Ile Ser Gln Arg Leu Arg
 965 970 975

Ile Tyr His Ser Ser
 980

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 <213> Homo sapiens

<220>
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 <223> Active portion of human Tal

<400> 7

Leu Lys Arg Lys Ser Leu Asp Thr Glu Ser Leu Gln Glu Met Ile Ser
 1 5 10 15

Glu Gln Arg Trp Ala Leu Ser Ser Leu Leu Gln Gln Leu Leu Lys Glu
 20 25 30

Lys Gln Gln Arg Glu Glu Glu Leu Arg Glu Ile Leu Thr Glu Leu Glu
 35 40 45

Ala Lys Ser Glu Thr Arg Gln Glu Asn Tyr Trp Leu Ile Gln Tyr Gln
 50 55 60

Arg Leu Leu Asn Gln Lys Pro Leu Ser Leu Lys Leu Gln Glu Glu Gly
 65 70 75 80

Met Glu Arg Gln Leu Val Ala Leu Leu Glu Glu Leu Ser Ala Glu His
 85 90 95

12

Tyr Leu Pro Ile Phe Ala His His Arg Leu Ser Leu Asp Leu Leu Ser
 100 105 110

Gln Met Ser Pro Gly Asp Leu Ala Lys Val Gly Val Ser Glu Ala Gly
 115 120 125

Leu Gln His Glu Ile Leu Arg Arg Val Gln Glu Leu Leu Asp Ala Ala
 130 135 140

Arg Ile Gln Pro Glu Leu Lys Pro Pro Met Gly Glu Val Val Thr Pro
 145 150 155 160

Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser Ala Pro Pro
 165 170 175

Ala Glu Leu Glu Val Gln Ala Ser Glu Cys Val Val Cys Leu Glu Arg
 180 185 190

Glu Ala Gln Met Ile Phe Leu Asn Cys Gly His Val Cys Cys Cys Gln
 195 200 205

Gln Cys Cys Gln Pro Leu Arg Thr Cys Pro Leu Cys Arg Gln Asp Ile
 210 215 220

Ala Gln Arg Leu Arg Ile Tyr His Ser Ser
 225 230

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Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser
 1 5 10 15

Ala Pro Pro Ala Glu Leu Glu Val Gln Ala Ser Glu Cys Val Val Cys
 20 25 30

Leu Glu Arg Glu Ala Gln Met Ile Phe Leu Asn Cys Gly His Val Cys
 35 40 45

Cys Cys Gln Gln Cys Cys Gln Pro Leu Arg Thr Cys Pro Leu Cys Arg
 50 55 60

Gln Asp Ile Ala Gln Arg Leu Arg Ile Tyr His Ser Ser
 65 70 75

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aaactgcagc cagagcagaa ctgagttctt catcc	35
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cctgcagagc tggaggtgc	19

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gtatgttatta cctctataag gcac	24	
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cacaatcatg acctgaataa gcc	23	
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<400> 22
cattcccaaca gctcccttat ac                                22

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ggaggtggag actacaagga c                                21

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ccgggatcca tggcggtgtc ggag                                24

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cccaagcttg gaaggatgcc gctctt                                26

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<400> 30
gccaggatcc agccagag                                         18

<210> 31
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cctcaactgt ggcgcgtct gctgctgcc                                         29

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ggcagcagca gacggcgcca cagttgagg                                         29

<210> 33
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<400> 33
cctgcagagc tggaggtgc                                         19

<210> 34
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Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser
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Ala Pro Pro

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cctcagctcc ctgctccagc agctgctcaa agagaagcag cagcgagagg aagagctccg 120
ggaaatcctg acggagttag aagccaaaag tgaaaccagg cagaaaaatt actggctgat 180
tcagtatcaa cggctttga accagaagcc cttgtcctt aagctgcaag aagagggat 240
ggagcgccag ctggtgccc tcctggagga gctgtcggt gagcactacc tgcccatctt 300
tgcgcaccac cgccctcac tggacctgct gagccaaatg agcccagggg acctggccaa 360
ggtgggcgtc tcagaagctg gcctgcagca cgagatcctc cggagagtc aggaactgct 420

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ggatgcagcc agatccagc cagagctgaa accaccaatg ggtgaggctcg tcaccctac 480
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 gcaggcctca gagtgtgtcg tgcgcctgga acgggaggcc cagatgatct tcctaactg 600
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 ttcctaact gtggccacgt ctgctgctgc cagcagtgct gccagccact ggcacactgc 180
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<400> 41
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<210> 42
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<220>
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<400> 42
 ttggaggguca gaagagagca g 21

<210> 43
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<220>
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<400> 43
guccaaagggu uccggagact t 21

<210> 44
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ttcagguuuc caaggccucu g 21

<210> 45
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<210> 47
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ugcugacuga gagcuguaat t 21

<210> 48
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uuacagcucu cagucagcat t 21

<210> 49
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<400> 49
aaugucgaga gucagucgut t

21

<210> 50
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acgacugacu cucgacauut t

21

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<220>
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<400> 51

Glu Val Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg
1 5 10 15

Pro Ser Ala Pro Pro Ala Glu
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aagaattcag aggtcgac ccctacgg

28

<210> 53
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<400> 53
aaggatccct ctgcaggggg agcgg

25